

RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/250,056C
Source: 1FW/6
Date Processed by STIC: 12/9/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/07/2006

PATENT APPLICATION: US/09/250,056C

TIME: 14:09:01

Input Set : N:\efs\12_07_06\09250056c_efs\407J-895030US_ST25.txt

Output Set: N:\CRF4\12072006\I250056C.raw

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3 <110> APPLICANT: Marks, James D
4   Poul, Marie A
6 <120> TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
8 <130> FILE REFERENCE: 407J-895030US
10 <140> CURRENT APPLICATION NUMBER: US 09/250,056C
11 <141> CURRENT FILING DATE: 1999-02-12
13 <150> PRIOR APPLICATION NUMBER: US 60/082,953
14 <151> PRIOR FILING DATE: 1998-04-24
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 246
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: scFv F5 amino acid sequence
29 <220> FEATURE:
30 <221> NAME/KEY: DOMAIN
31 <222> LOCATION: (31)..(35)
32 <223> OTHER INFORMATION: VH-CDR1
34 <220> FEATURE:
35 <221> NAME/KEY: DOMAIN
36 <222> LOCATION: (50)..(66)
37 <223> OTHER INFORMATION: VH-CDR2
39 <220> FEATURE:
40 <221> NAME/KEY: DOMAIN
41 <222> LOCATION: (99)..(108)
42 <223> OTHER INFORMATION: VH-CDR3
44 <220> FEATURE:
45 <221> NAME/KEY: DOMAIN
46 <222> LOCATION: (157)..(170)
47 <223> OTHER INFORMATION: VL-CDR1
49 <220> FEATURE:
50 <221> NAME/KEY: DOMAIN
51 <222> LOCATION: (186)..(192)
52 <223> OTHER INFORMATION: VL-CDR2
54 <220> FEATURE:
55 <221> NAME/KEY: DOMAIN
56 <222> LOCATION: (225)..(235)
57 <223> OTHER INFORMATION: VL-CDR3
59 <400> SEQUENCE: 1
61 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
62 1           5           10           15

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65 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
66          20          25          30
69 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
70          35          40          45
73 Ser Ala Ile Ser Gly Arg Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val
74          50          55          60
77 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
78 65          70          75          80
81 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
82          85          90          95
85 Ala Lys Met Thr Ser Asn Ala Phe Ala Phe Asp Tyr Trp Gly Gln Gly
86          100          105          110
89 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
90          115          120          125
93 Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
94          130          135          140
97 Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser
98 145          150          155          160
101 Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln Leu Pro
102          165          170          175
105 Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser
106          180          185          190
109 Gly Val Pro Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser
110          195          200          205
113 Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
114          210          215          220
117 Gln Ser Tyr Asp Ser Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr
118 225          230          235          240
121 Lys Leu Thr Val Leu Gly
122          245
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 242
127 <212> TYPE: PRT
128 <213> ORGANISM: Artificial
130 <220> FEATURE:
131 <223> OTHER INFORMATION: scFv C1 amino acid sequence
134 <220> FEATURE:
135 <221> NAME/KEY: DOMAIN
136 <222> LOCATION: (31)..(35)
137 <223> OTHER INFORMATION: VH-CDR1
139 <220> FEATURE:
140 <221> NAME/KEY: DOMAIN
141 <222> LOCATION: (50)..(66)
142 <223> OTHER INFORMATION: VH-CDR2
144 <220> FEATURE:
145 <221> NAME/KEY: DOMAIN
146 <222> LOCATION: (99)..(108)
147 <223> OTHER INFORMATION: VH-CDR3
149 <220> FEATURE:

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Output Set: N:\CRF4\12072006\I250056C.raw

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150 <221> NAME/KEY: DOMAIN
151 <222> LOCATION: (157)..(167)
152 <223> OTHER INFORMATION: VL-CDR1
154 <220> FEATURE:
155 <221> NAME/KEY: DOMAIN
156 <222> LOCATION: (184)..(190)
157 <223> OTHER INFORMATION: VL-CDR2
159 <220> FEATURE:
160 <221> NAME/KEY: DOMAIN
161 <222> LOCATION: (223)..(231)
162 <223> OTHER INFORMATION: VL-CDR3
164 <400> SEQUENCE: 2
166 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
167 1 5 10 15
170 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
171 20 25 30
174 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
175 35 40 45
178 Ser Ser Ile Ser Gly Ser Ser Arg Tyr Ile Tyr Tyr Ala Asp Ser Val
179 50 55 60
182 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
183 65 70 75 80
186 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
187 85 90 95
190 Ala Lys Met Asp Ala Ser Gly Ser Tyr Phe Asn Phe Trp Gly Gln Gly
191 100 105 110
194 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
195 115 120 125
198 Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro Ser Phe
199 130 135 140
202 Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser
203 145 150 155 160
206 Pro Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
207 165 170 175
210 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
211 180 185 190
214 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
215 195 200 205
218 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
219 210 215 220
222 Tyr Asn Ser Tyr Pro Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile
223 225 230 235 240
226 Lys Arg
230 <210> SEQ ID NO: 3
231 <211> LENGTH: 738
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial
235 <220> FEATURE:
236 <223> OTHER INFORMATION: nucleic acid encoding scFv F5 Ab

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238 <400> SEQUENCE: 3
239 caggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc      60
241 tcctgtgcag cctctggatt cacctttcgc agctatgccca tgagctgggt ccgccagggt      120
243 ccagggaagg ggctggagtg ggtctcagct attagtgggtc gtggtgataa cacatactac      180
245 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
247 ctgcaaatga acagcctgag agccgaggac acggccggtt attactgtgc gaaaatgaca      300
249 agtaacgcgt tcgcatttga ctactggggc cagggaaccc tggtcaccgt ctctcagggt      360
251 ggaggcgggt caggcggagg tggctctggc ggtggcggat cgcagtctgt gttgacgcag      420
253 ccgccctcag tgtctggggc cccaggggcag agggtcacca tctcctgcac tgggagcagc      480
255 tccaacatcg gggcagggtta tgggtgtacac tgggtaccagc agcttcaggg aacagccccc      540
257 aaactcctca tctatggtta cccaatcgg ccctcagggg tccctgaccg attctctggc      600
259 ttcaagtctg gccacctcagc ctccctggcc atcactgggc tccaggctga ggatgaggct      660
261 gattattact gccagtccta tgacagcagc ctgagtgggt ggggtgttcg cggagggacc      720
263 aagctgaccg tgctaggt                                     738
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 726
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Nucleic acid encoding scFv C1 amino acid sequence
275 <220> FEATURE:
276 <221> NAME/KEY: misc feature
277 <222> LOCATION: (111)..(111)
278 <223> OTHER INFORMATION: N = A, C, G, or T
280 <400> SEQUENCE: 4
W--> 281 caggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc      60
283 tcctgtgcag cctctggatt caccttttagc agctatgccca tgggctgggt ccgccagggt      120
285 ccagggaagg ggctggagtg ggtctcatca attagtggca gtagtagata catatattac      180
287 gcagactccg tgaagggccg gttcaccatc tcccgagaca attccaagaa cacgctgtat      240
289 ctgcaaatga acagcctgcg agccgaggac acggccggtt attactgtgc gaaaatggat      300
291 gcttcgggga gttattttta tttctggggc cagggcaccc tggtcaccgt ctctcagggt      360
293 ggaggcgggt caggcggagg tggctctggc ggtggcggat cggaaacgac actcacgcag      420
295 tctccatcct tcctgtctgc atttgttaga gacagaatca ccatcacttg ccgggccagt      480
297 ccgggcatta ggaattattt agcctgggtat cagcaaaaac cagggaagc ccctaagctc      540
299 ctgatctatg ctgcatctac tttgcaaagt ggggtcccat caaggttcag cggcagtgga      600
301 tctgggacag attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat      660
303 tattgtcaac aatataatag ttaccctctc agtttcggcg gagggaccaa ggtggagatc      720
305 aaacgt                                     726
308 <210> SEQ ID NO: 5
309 <211> LENGTH: 5
310 <212> TYPE: PRT
311 <213> ORGANISM: Artificial
313 <220> FEATURE:
314 <223> OTHER INFORMATION: translocation sequence
316 <400> SEQUENCE: 5
318 Arg Glu Asp Leu Lys
319 1      5
322 <210> SEQ ID NO: 6
323 <211> LENGTH: 4

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Input Set : N:\efs\12_07_06\09250056c_efs\407J-895030US_ST25.txt

Output Set: N:\CRF4\12072006\I250056C.raw

324 <212> TYPE: PRT
325 <213> ORGANISM: Artificial
327 <220> FEATURE:
328 <223> OTHER INFORMATION: translocation sequence
330 <400> SEQUENCE: 6
332 Arg Glu Asp Leu
333 1
336 <210> SEQ ID NO: 7
337 <211> LENGTH: 4
338 <212> TYPE: PRT
339 <213> ORGANISM: Artificial
341 <220> FEATURE:
342 <223> OTHER INFORMATION: translocation sequence
344 <400> SEQUENCE: 7
346 Arg Asp Glu Leu
347 1
350 <210> SEQ ID NO: 8
351 <211> LENGTH: 4
352 <212> TYPE: PRT
353 <213> ORGANISM: Artificial
355 <220> FEATURE:
356 <223> OTHER INFORMATION: translocation sequence
358 <400> SEQUENCE: 8
360 Lys Asp Glu Leu
361 1

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/250,056C

DATE: 12/07/2006
TIME: 14:09:02

Input Set : N:\efs\12_07_06\09250056c_efs\407J-895030US_ST25.txt
Output Set: N:\CRF4\12072006\I250056C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 111

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8

VERIFICATION SUMMARY

DATE: 12/07/2006

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Input Set : N:\efs\12_07_06\09250056c_efs\407J-895030US_ST25.txt

Output Set: N:\CRF4\12072006\I250056C.raw

L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:60